

Figure 1

1' MAVALRGLGWRFRWRTQAVAGGVARGAARGAAAGORDYDLLVVGSGGLACAKEAAQLGR
 ****...*****
 1" MNGPEDLPKSYDYDLIIIGGSGGLAAAKEAAQYGK
 FAD-binding region (ADP)

61' KVAVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH
 ** *...* *...*****
 37" KVMVLDFVTPPLGTRWGLGGTCVNVGCIPKKLMHQAALLGQALQDSRNYGWKVEETVKH

Reduction active center

121' DWRKMAEAVQNHVKSINWGHVQLQDRVKYFNIKASFVDEHTVCGVAKGGKEILLSADH
 ** *...* *...*****
 97" DWDRMIEAVQNHIGSLNWGYRVALREKKVYENAYGQFIGPHRIKATNNKGKEKIYSAES

181' IIIATGGRPRYPHTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTIGIGLD
 ..*****.*** *...* *...*****
 157" FLIATGERPRYLG-IPGDKEYCISDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLG
 NADPH-binding domain

241' TTIMMRSIPLRGFDQOMSSMVIEHMASHGTRFLRGCAPSRVRL---PDGQLQVTWEDST
 ..*...*** *...* *...* *...* *...* *...* *...* *...* *...* *...* *...*
 216" VTVMVRSILLRGFDQDMANKIGEHEHGIKFIRQFVPIKVEQIEAGTPGRLRVVAQSTN

298' TGKEDTGTFTDVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDV
 ... *...* *...* *...* *...* *...* *...* *...* *...* *...* *...*
 276" SEEIIEGEYNTVMLAIGRDACTRKIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDI
 FAD-binding region (Flavin)

358' VEGRPELTPTAIMAGRLLVQRLFGGSSDLMYDYNVPTTVFTPLEYGCVGLSEEEAVARHG
 ... ***** *...*****
 336" LEDKVELTPVAIQAGRLLAQRLYAGSTVKCDYENVPTTVFTPLEYGCGLSEEKAVEKFG

418' QEHVEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPTAGAGPAFSLAPTOGEVTQGFAL
 ..*****.*** *...* *...* *...* *...* *...* *...* *...* *...* *...*
 396" EENIEVYHSYFWPLEWTIPSRDNNKCYAKIICNTKDNERVVG-FHVLGPNAGEVTQGFAL

478' GIKCGASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCSecysG
 ..*****.*** *...*****
 455" ALKCGLTQKQLDSTIGIHPVCAEVFTTSLSVTKRSGASILQAGCsecysG

09/830706-080704

Figure 2

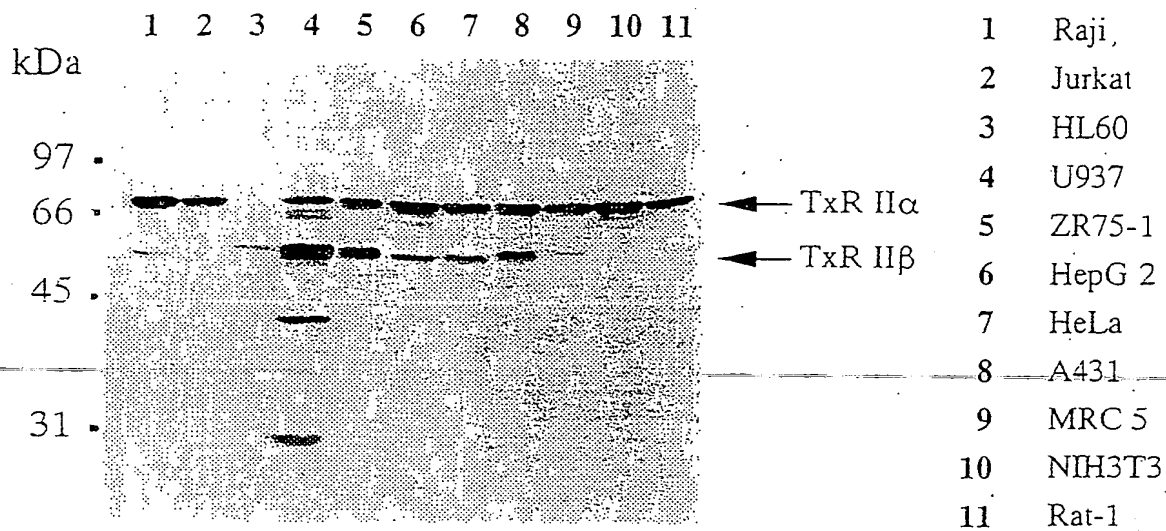


Figure 3

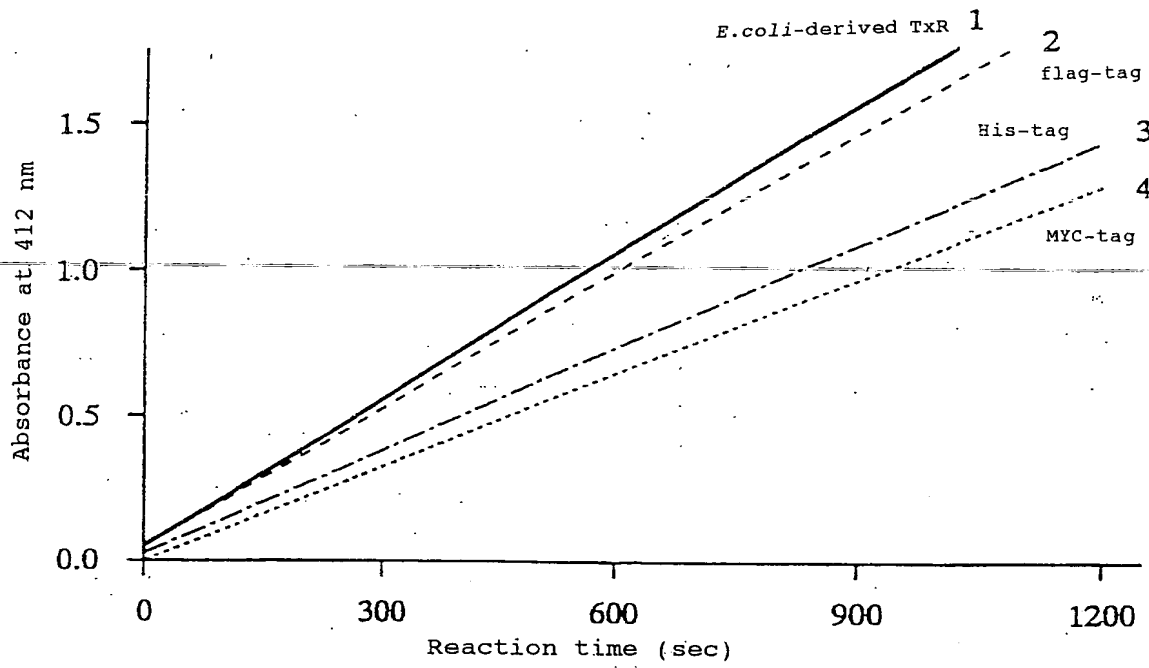


Figure 4

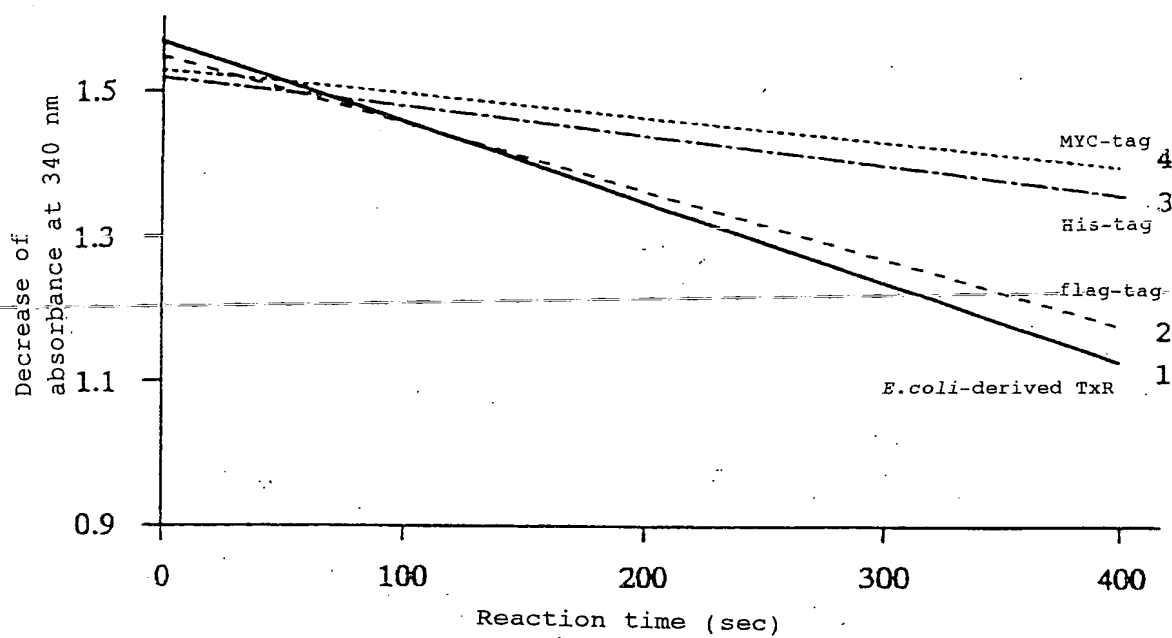


Figure 5

